

A Gene for Resistance to Common Blight  
(Xanthomonas campestris pv. phaseoli)

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In 1985, a small packet of seed of a Co-60 mutant of Zarya snap bean, an early flowering, white seeded dwarf bush variety, was obtained from Ivan Poriazov of the Maritsa Vegetable Crops Research Institute of Bulgaria. This mutant, according to information published in Mutation News and the 1983 volume of BIC, possessed a measure of field and greenhouse resistance to 3 out of 4 of the Bulgarian strains of common bean blight, Xanthomonas campestris pv. phaseoli.

Upon receiving the seed of the line A-8-40, Dr. A. W. Saettler, USDA plant pathologist at M.S.U. tested a sample of seedlings in the greenhouse for reaction to a local Mich. isolate of the common blight organism, and to a fuscous blight isolate. The plants were variable in their response, but happily, several seedlings proved moderately to highly tolerant to both isolates. Repeated testing of subsequent samples confirmed the initial responses.

We point out that the plant response induced by this mutant is one of significant retardation of development of spreading lesions and collapse of leaf tissue. It does not, apparently, protect against seed becoming infected.

Subsequently, with progeny plants descendant from the more tolerant seedlings, we initiated a crossing program to incorporate the resistant gene or genes into beans representing several commercial seed classes. Concurrently, we have screened parents,  $F_2$  populations, a limited number of backcrosses, and a group of selected  $F_3$  families with a single isolate of X. c. phaseoli, (Mich. #5) in order to test plausible genetic hypotheses.

Two inoculation and scoring procedures were used: in one, a spray-to-runoff inoculation method on seedling plants in the third trifoliate leaf stage, and a 1-9 scoring system based upon lesion development were employed; in the second case, inoculation was done by use of a hypodermic syringe, injecting a bacterial suspension into the underside of each of the leaflets of the expanded first trifoliate leaf, using a 1 to 5 scale (as illustrated in slides presented). Both methods produced similar numerical results, although we find that the syringe method produces discrete lesions which can be more objectively scored.

We classified as resistant all plants displaying scores of 1 or 2, since the resistant parent displayed only those scores; all other scores were treated as susceptibles. Susceptible parents were scored as 4 or 5, or as 7, 8 or 9, dependent upon the scale used. For each cross, 30  $F_3$  families were selected, 10 from resistant  $F_2$  plants, and 20 from susceptible  $F_2$ 's. These families were inoculated by the syringe method and scored as true-breeding resistant, and as segregating or non-segregating susceptibles. This categorization was based upon the hypothesis of a recessive gene for resistance.

This is a preliminary report of results obtained with crosses involving two advanced navy bean selections, N84004 and N84024, the latter approved for release as a commercial variety.

The numerical results are given in the accompanying table (Table 1).

The data support the hypothesis of a single major recessive gene conferring resistance. Because of the occurrence of intermediates, however, we cannot rule out the possibility of modifying genes; and, in a wider array of crosses, now being screened, the possibility of genic interaction cannot be excluded.

We have found no association of the resistance factor with earliness to flower, determinate vs. indeterminate growth, plant architecture, or with flower color. We have been able to select for resistant plants in field nurseries in  $F_2$  and  $F_3$  generations, and are hopeful we can introduce this factor into both small-seeded and large-seeded gene pools. Interestingly, we did not encounter dominant  $Dl_1$   $Dl_2$  interaction effects in the  $F_1$  generation of A-8-40-line (snap bean) by navy bean crosses, or A-line by kidney or cranberry crosses. We have, however, encountered a recessive dwarf lethality expressed in  $F_2$  and  $F_3$  generations.

Table 1

Cross #	Total # Plants	# Resist.	# Susc.	Expected # on 3:1 hypothesis		Chi- Square	Prob.
				Resist.	Susc.		
<u>A 118-F<sub>2</sub></u>							
Test 1	183	48	135	46	137	0.147	(.50-.75)
Test 2	98	19	79	24	74	1.646	(.10-.25)
<u>A 119-F<sub>2</sub></u>							
Test 1	207	40	167	52	155	3.55	(.05-.10)
Test 2	98	22	73	24	71	0.172	(.50-.75)
<u>Pooled Backcrosses</u>							
BC to Resist.							
Parent	27	14	13	13.5	13.5	--	--
BC to Susc.							
Parent	34	5	29	0	34	--	--

Selected  $F_3$  Family Analysis

		# families expected Resist.	# families expected Susc.	# families Segreg.	# families Non-Segreg.
<u>Cross A 118 (Selected families)</u>					
# families expected:	30	10	20	13.33	7.67
# families observed:	30	9	21	14	7
<u>Cross A 119 (Selected families)</u>					
# families expected:	30	10	20	12.67	6.33
# families observed:	30	11	19	12	7